

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:32:46 ; Search time 46.42 Seconds

(Without alignments)
758.135 Million cell updates/sec

Title: US-09-653-755A-6

Perfect score: 2487

Sequence: 1 EVQLQSGPELVKPGASVMI.....YLKTTISRSRPGKGNHHHH 462

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-68:*
2: p1r1:*
3: p1r2:*
4: p1r3:*
5: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2190.5	88.1	474	1 G2MS11	Ig gamma-2b chain
2	2135.	85.8	475	2 S01321	Ig gamma-2b chain
3	1835.	73.8	469	2 S37483	Ig gamma-2a chain
4	1832.5	73.7	446	2 S40295	Ig gamma-2a chain
5	1797	72.3	405	1 G2MSBM	Ig gamma-2b chain
6	1439	57.9	444	2 PCA436	monoclonal antiod
7	1419	57.1	330	1 G2MSA	Ig gamma-2a chain
8	1414	56.9	399	1 G2MSAM	Ig gamma-2a chain
9	1385.5	55.7	335	1 G2MSAB	Ig gamma-2a chain
10	1326.5	53.3	333	2 PS0018	Ig gamma-2a chain
11	1321.5	53.1	472	2 S31459	Ig gamma-1 chain
12	1286.5	51.7	470	2 S22080	Ig heavy chain pre
13	1202.5	48.4	329	2 S00847	Ig gamma-2c chain
14	1170	47.0	329	1 G3MSC	Ig gamma-3 chain C
15	1159	46.6	338	1 G3MSM	Ig gamma-3 chain C
16	1150	46.2	324	1 G1MS	Ig gamma-1 chain C
17	1145	45.3	333	1 G1MSM	Ig gamma-1 chain C
18	1112	44.7	326	2 PS0017	Ig gamma-1 chain C
19	1100	44.2	322	2 PS0019	Ig gamma-1 chain C
20	1087	43.7	350	1 GHU	Ig gamma-2a chain
21	1080.5	43.4	323	1 GHRB	Ig gamma-1 chain C
22	1080.5	43.4	329	1 G2GP	Ig gamma-2 chain C
23	1072.5	43.1	377	2 A60764	Ig gamma-3 chain C
24	1072.5	43.1	377	2 A23511	Ig gamma-3 chain C
25	1059	42.6	326	1 G2HU	Ig gamma-2 chain C
26	1058	42.5	328	2 I47159	Ig gamma-4 chain C
27	1054.5	42.4	327	1 G4HU	Ig gamma-4 chain C
28	1049	42.2	328	2 I47160	Ig gamma-2b chain
29	1028	41.3	328	2 I47161	Ig gamma-3 chain C

30	1023.5	41.2	308	2 C30554	Ig heavy chain C r
31	1022	41.1	328	2 I47158	Ig gamma-1 chain c
32	1014.5	40.8	246	2 S38950	Ig gamma chain - m
33	1008.5	40.6	548	2 S38864	Ig epsilon chain C
34	987.5	39.7	327	2 S06611	Ig gamma-2 chain C
35	918.5	36.9	374	2 S69339	Ig heavy chain V r
36	884	35.5	277	2 I47162	Ig gamma-4 chain c
37	855.5	34.4	231	2 PC4155	Ig gamma-2b chain C
38	819	32.9	549	2 S04845	Ig heavy chain pre
39	818.5	32.9	627	2 S14683	Ig mu chain precu
40	781.5	31.4	255	4 S31866	Ig gamma-1 chain C
41	778.5	31.3	221	2 S49220	Ig gamma-1 chain -
42	778	31.3	214	2 PC4202	monoclonal antiod
43	774.5	31.1	213	2 S68213	Ig heavy chain (Ma
44	774.5	31.1	234	2 PT0207	Ig gamma chain C r
45	771.5	31.0	289	1 G3H0W1	Ig gamma-3 heavy c

ALIGNMENTS

RESULT 1
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26232; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, R.J.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
A:Reference number: S25057
A:Accession: S25057
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Oyata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro
A:Reference number: A02157; MUID:80120716
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b
A:Reference number: A26235; MUID:80081501
A:Accession: A26235
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno
A:Reference number: A26232; MUID:80081502
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g
A:Reference number: A26233; MUID:82173203
A:Accession: A26233
A:Contents: b allele
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah
J. Biol. Chem. 269, 12345-12350, 1994

A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359
A:Accession: A53598
A:Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
F:157-222/Domain: immunoglobulin homology <IM1>
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.1%; Score 2190.5; DB 1; Length 474;
Best Local Similarity 91.2%; Pred. No. 4.1e-123;
Matches 415; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 1 EVOLQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 60
DB 20 QVLOQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 79
QY 61 SPKFKGKATLVYDKSSSTAYMELRSLTSDSAVYVCARRAGAYFPDYGQGTTLVYSSAK 120
DB 80 NEKFKGKATLVYDKSSSTAYMELRSLTSDSAVYVCARRAGAYFPDYGQGTTLVYSSAK 139
QY 121 TTPPSVYPLAPGCGDTGSSVTGLGCLVKGFPESVTVTNSSGSLSSVHTF-PALLQSL 179
DB 140 TTPPSVYPLAPGCGDTGSSVTGCGVKGFPESVTVTNSSGSLSSVHTLQALLOSL 199
QY 180 YTMSSSVYTPSSVPSQVTCVAHPASTTYDKKLEPSGISTINPCPKCKCHKCPA 239
DB 200 YTMSSSVYTPSSVPSQVTCVAHPASTTYDKKLEPSGISTINPCPKCKCHKCPA 259
QY 240 NLEGGPSVFPFPNPKIDVLMISLTPKVTGVVVDSEDDPVOISMVNVNVEVHTAQTOT 299
DB 260 NLEGGPSVFPFPNPKIDVLMISLTPKVTGVVVDSEDDPVOISMVNVNVEVHTAQTOT 319
QY 300 REDYNSTIRVSTLPIQHDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 359
DB 320 REDYNSTIRVSTLPIQHDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYILP 379
QY 360 PPAEQLSRKDVSLTCLVGFNPBGDISVEMTNGHTEENKDPAPVLDSDGSFYISKLM 419
DB 380 PPAEQLSRKDVSLTCLVGFNPBGDISVEMTNGHTEENKDPAPVLDSDGSFYISKLM 439
QY 420 KTSKWEKTDSPFCNVNHEGLKNYLLKTTISRSPGK 454
DB 440 KTSKWEKTDSPFCNVNHEGLKNYLLKTTISRSPGK 474

RESULT 2
Ig gamma-2b chain precursor - mouse
S01321
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321

R:de Waale, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-Lymphoid cells of mouse recombinant immunoglobulin directed at

A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475

A:Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781
A>Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <KAT>
F:159-223/Domain: immunoglobulin homology <IMW>

Query Match 85.8%; Score 2135; DB 2; Length 475;
Best Local Similarity 88.4%; Pred. No. 8.1e-120;
Matches 403; Conservative 15; Mismatches 36; Indels 2; Gaps 1;

QY 1 EVOLQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 60
DB 20 QVLOQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 79
QY 61 SPKFKGKATLVYDKSSSTAYMELRSLTSDSAVYVCARRAGAYFPDYGQGTTLVYSS 118
DB 80 NEKFKGKATLVYDKSSSTAYMELRSLTSDSAVYVCARRAGAYFPDYGQGTTLVYSSA 139
QY 119 AKTTPSVYPLAPGCGDTGSSVTGLGCLVKGFPESVTVTNSSGSLSSVHTFPALLQSG 178
DB 140 AKTTPSVYPLAPGCGDTGSSVTGLGCLVKGFPESVTVTNSSGSLSSVHTFPALLQSG 199
QY 179 LVTMSSSVYTPSSVPSQVTCVAHPASTTYDKKLEPSGISTINPCPKCKCHKCPA 238
DB 200 LVTMSSSVYTPSSVPSQVTCVAHPASTTYDKKLEPSGISTINPCPKCKCHKCPA 259
QY 239 NLEGGPSVFPFPNPKIDVLMISLTPKVTGVVVDSEDDPVOISMVNVNVEVHTAQTOT 298
DB 260 NLEGGPSVFPFPNPKIDVLMISLTPKVTGVVVDSEDDPVOISMVNVNVEVHTAQTOT 319
QY 299 HREDYNSTIRVSTLPIQHDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 358
DB 320 HREDYNSTIRVSTLPIQHDMMSGKEFKCKVNNKDLPSPIERTISKIGLVAPQVYIL 379
QY 359 PPAEQLSRKDVSLTCLVGFNPBGDISVEMTNGHTEENKDPAPVLDSDGSFYISKLM 418
DB 380 PPAEQLSRKDVSLTCLVGFNPBGDISVEMTNGHTEENKDPAPVLDSDGSFYISKLM 439
QY 419 KTSKWEKTDSPFCNVNHEGLKNYLLKTTISRSPGK 454
DB 440 KTSKWEKTDSPFCNVNHEGLKNYLLKTTISRSPGK 475

RESULT 3
S37483
Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducaucel, F.F.D.
Submitted to the EMBL Data Library, February 1993

A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DDUC>
A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMW>

Query Match 73.8%; Score 1835; DB 2; Length 469;
Best Local Similarity 75.7%; Pred. No. 5.3e-102;
Matches 345; Conservative 44; Mismatches 59; Indels 8; Gaps 3;

QY 1 EVOLQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 60
DB 20 QVLOQSGPELVKPGASVWISCRSAFTFTENTVHWKQSHGESLEWIGINPYGGSIF 79

Qy	61	SPKEFGKATLTITDKSSNTHAAWELJSTEDSDAIVVYCARAG--AYFDWGGGTTLTWSS	118
Db	80	NENFEGKATLTIVDTSSSTAYIMQLSITJSEDIAYVYCCARAMGATALLDWMGGTTLTWSS	139
Qy	119	AKTTPPSVYPLAPGCGDITGSSVTLGCLVKGGYFPECSVWTWMSGSLSSVHFFPALLOG	178
Db	140	AKTTPASVYPLAPVCGDITGSSVTLGCLVKGGFPEPVPYITLWMSGSLSSVHFFPALDSD	199
Qy	179	LYTMSSSVTVPBSSTWPSQTVTCSVAHPASSTTVDKRLFESGDISTINPCRPKECHKCPA	238
Db	200	LYTLSSSVTWVSSSTWPSQITCNVAHPASSTKVDKRIEPRGP--TlKPCPCP---KCPA	253
Qy	239	PNLEGGPSVFITPPNINKDYLMISLPKTYCVVVDYSEDDPDVQISMFVNANVHHAQIOT	298
Db	254	PNLGGPSVFITPPKIKDVLMLISPIYTCVVVDYSEDDPDVQISMFVNANVEHHAQIOT	313
Qy	299	HREDNSTIRAVSTPLIOHODMMSGKEFKCKYNNKDLPSPIERTISKIGLRAPOVYTL	358
Db	314	HREDNSTIRAVSALPLIOHODMMSGKERCKYNNKDLPLPIERTISKPGSVRAPOVYTL	373
Qy	359	PPPAQOLSRKDYSLTCLVYVGFNPBGDISVEMTNSNGTHEENYKDTAVALDSDGSYFYTSKLN	418
Db	374	PPPEDEMTKRQYTLTLCVMTDFMPEDIVYEMTNNKGTELNYKNTPEVLDSDGSYFMYSKLR	433
Qy	419	MKTSWEKTDTSFCVNRHDEGLKNYILKKTISRSPGK	454
Db	434	VEKKMMYERNYSYSCVHIEGLHNNHTTKSFSRTPGK	469

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RESULT      4
S40295      I $\gamma$  gamma-2a chain (mb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klebett, S., Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; B
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: I $\gamma$  gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-210/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMN>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:2-2-96, 144-199, 261-371, 367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224, 227, 229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

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	Query Match	73.7%;	Score 1832.5;	DB 2;	Length 446;	
	Best Local Similarity	75.9%;	Pred. No. 7.1e-102;			
	Matches 344;	Conservative 44;	Mismatches 58;	Indels 7;	Gaps 3;	
QY	1 EVQLDQSPELTKPCASVWISCRITSAFTTETVMHWKOSHESLTLEIGINLPYYGGSTF 60	:::::::::::::::::::::	:::::::::::::	:::::	:	:
Dd	1 QIOLQSGELTRPQASVSKSCAGSYFTFDYYIHVKORPEGEGLMGIWPGSGNTKY 60	:::::::::::::::::::	:::::::::::::	:::::	:	:
QY	61 SPKFQKATLVLDKSSSTRAYMELRSLTSDDSAVYICARACAGLYEDYWGQTLLIVSSAK 120	:::::::::::::::::::::	:::::::::::::	:::::	:	:
Dd	61 NEKFGKATLVDTSSSTRAYMLSSLTSDSAAVFCA -GGGFADMDYQGGSIVTVSSAK 119	:::::::::::::::::::::	:::::::::::::	:::::	:	:

[illegible]

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RESULT 5
G2MSBM
Ig gamma-2b chain C region, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Dec-1992 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: C02154; A02158; B02157
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A:Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin
A:Reference number: A02154; MUID:82222190
A:Accession: C02154
A:Molecule type: DNA
A:Residues: 335-405 <YAM>
A:Cross-references: GB:J00462
R:Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Warr
Cell 26, 19-27, 1981
A:Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma
A:Reference number: A02158; MUID:82115295
A:Accession: A02158
A:Molecule type: DNA
A:Residues: 335-378 <ROG>
A:Note: The translation of the first exon of the membrane-bound segment is given
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obara, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from
A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: B02157
A:Molecule type: DNA
A:Residues: 1-335,'K' <YA2>
A:Comment: The sequence of residues 1-334 was assumed to be identical with the corres
A:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The
hat it contains an alternative 3' end, encoded in separate exons, that is homologous
C:Genetics:
A:Introns: 1/1, 98/1; 120/1; 230/1, 335/1; 378/3
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F:143-212/Domain: immunoglobulin homology <IMM>
F:353-369/Domain: transmembrane #Status predicted <TM>
F:370-405/Domain: intracellular #Status predicted <INT>
F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match	72.3%	Score 1797	DB 1	Length 405
Best Local Similarity	100.0%	Pred. No. 8	1e-100	
Matches 335	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	119	AKTTPSVYPLAPGGGDDTSSVTLGCLVKGFFPESVYVTWMSGLSSSVHFFPALLQSG	178
Db	1	AKTTPSVYPLAPGGGDDTSSVTLGCLVKGFFPESVYVTWMSGLSSSVHFFPALLQSG	60
Qy	179	LYTMSSTVTPSSPTQOTVTCVAHPASSSTTVDKLEPSGPISTINPCPCKECHKCPA	238
Db	61	LYTMSSTVTPSSPTQOTVTCVAHPASSSTTVDKLEPSGPISTINPCPCKECHKCPA	120
Qy	239	PNLEGGPSVFIFPPNIKQVLMISLTPKVTQVVDVSEDDPDVQISMFVNNVEVHTAQOT	298
Db	121	PNLEGGPSVFIFPPNIKQVLMISLTPKVTQVVDVSEDDPDVQISMFVNNVEVHTAQOT	180
Qy	299	HREDYNSTIRVSVTLPIQHODMMSGKEFKCKVNNKDLSPLERTTSIKIGLVARQVYL	358
Db	181	HREDYNSTIRVSVTLPIQHODMMSGKEFKCKVNNKDLSPLERTTSIKIGLVARQVYL	240
Qy	359	PPPAEQLSRKQVSLTCLVVGFRNPGLISYEWTMSGHTENYKDTAVLDSDGSYFIYSKLN	418
Db	241	PPPAEQLSRKQVSLTCLVVGFRNPGLISYEWTMSGHTENYKDTAVLDSDGSYFIYSKLN	300
Qy	419	MKTSWEKTDSPSCVNRHGLKNYLLKKTISRPG	453
Db	301	MKTSWEKTDSPSCVNRHGLKNYLLKKTISRPG	335

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Arashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyry
A:Reference number: JCS810; MUID:98063277
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKKA>
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:251-320/Domains: Immunoglobulin homology <IMM>
F:22/Disulfide bonds: Interchain (to 98) #status predicted
F:99/Disulfide bonds: Interchain (to 109) #status predicted

Query Match	57.98;	Score 1439;	DB 2;	Length 444;
Best Local Similarity	59.38;	Pred. No. 1.7e-78;		
Matches 271; Conservative	68;	Mismatches 102;	Indels 16;	Gaps 6;

[illegible]

QY 418 NKKTSRWEKTDVSCNVRHEGKLNYYLKKTTSRSPGK 454
 QY 408 NVQKSNWEAGNFTFSCVLAHEGLNHNHTERKSLSHSPGK 444
 Db 348 IPPPEQMAKKDKVSLTTCMTDPFEDITVEVOMQGNQPAENKNTOPIMDTGOSTVYVSKL 407
 QY 358 IPPPEQOLSRKDDVSLTLCVWGNPGDISEVMTSNHEENTKDAIPVLDGSGSYVSKL 417

RESULT	7
G2MSA	

C/Species: Balb/c-murine (mouse-model)
C/Date: 30-Sep-1980 #sequence_revision 01-Sep-1981 #text-change 16-Jun-2000
C/Accession: A02152; A32657; A32658
R:Skorav, J.L.; Aufrey, C.; Rougeon, F.
Nucleic Acids Res. 8 3143-3155, 1980
A>Title: Structure of the constant and 3' untranslated regions of the murine Balb/C g
A/Reference number: A02152; MUID:81076554
A/Accession: A02152
A/Molecule type: mRNA
A/Residues: 1-330 <STK>
A/Cross-references: YB:V00798; NID:951835; PIDN:CAA24178.1; PID:g1333984
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A>Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and
A/Reference number: A32657; MUID:81198976

A:Accession: A32657
A:Molecule type: DNA
A:Residues: 1-330 <YAM>
A:Cross-references: GB:J00470
A:Note: The sequence was determined from the germline gene
R:Ollio, R.; Aulifrey, C.; Morchamps, C.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A:Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests
A:Reference number: A32658: MUID:81233894

A:Accession: A32658
A:Molecule type: DNA
A:Residues: 1-330 <OLL>
A:Note: The sequence was determined from the germline gene
A:Note: Lys-330 is removed posttranslationally
R:Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Biochem. 43, 423-435, 1974
A:Title: Determination of the primary structure of a mouse Ig2a immunoglobulin: amino

A:Contents: annotation; myeloma protein MOPC 173
A:Note: this is one paper in a series reporting the sequence; for additional references
A:Note: this sequence differs from that shown at a number of positions
R:de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A:Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. I
A:Reference number: A32660; MIMD:73056887
A:Contents: annotation; MOPC 173, disulfide bonds
C:Genetics:
A:Introns: 1/1; 98/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; immunoglobulin homology <IM1>
F:20-84/Domain: immunoglobulin homology <IM1>
F:98-113/Region: hinge
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:15-23/Disulfide bonds: interchain (to light chain) #status experimental
F:27-82,114-204,230-308/Disulfide bonds: #status experimental
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match	57.1%	Score 1419;	DB 1;	Length 330;
Best Local Similarity	78.6%	Pred. No. 1.8e-77;		
Matches 264; Conservative	30;	Mismatches 36;	Indels 6;	Gaps 2;

Query 119 AKTTPSVYPLAPGCGPTGSSVTGLGVKGYPEPESVTVMNSSLSSSVHTFPALLQSG 178
1 AKTAPSVYPLAPVPCGGTSSVTGLGVKGYPEPVTLLTNSSSLSSGVTFFPAVLQSD 60
Db 1 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
179 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
61 LYTSSSVTVTSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 114
Qy 239 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 298
115 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 174
Qy 299 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 358
175 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 234
Db 359 PPAEQLSRKDVSLTCLVGVFNPDISVETWSNGHTEBNYKDTAPVLDSDGSYFYSKLN 418
235 PPPEEMTKKQVTLTCVTDPEMDIYEWMTNNGKTELNTPEVLDSDGSYFYSKLR 294
Qy 419 MKTSKMEKTDSEFCNVNHEGLKNTYLLKTTISRSPG 454
295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 330
Db 295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 330

RESULT 8
G2MSAM
Ig gamma-2a chain C region, membrane-bound form - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Feb-1984 #sequence.revision 31-Mar-1991 #text.change 16-Jul-1999
C:Accession: A02154; B32657; I57809
R:Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A:Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin A:Reference number: A02154; MUID:82222190
A:Accession: A02154
A:Molecule type: DNA
A:Residues: 329-399 <YAM>
A:Cross-references: GB:J00471
R:Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and env A:Reference number: A32657; MUID:81198976
A:Accession: B32657
A:Molecule type: DNA
A:Residues: 1-329, 'K' <YA2>
R:Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin gamma A:Reference number: I57809; MUID:90097953
A:Accession: I57809
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 373-399 <RES>
A:Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C:Comment: The sequence of residues 1-328 was assumed to be identical with the counterpart C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The material it contains an alternative 3' end, encoded in separate exons, that is homologous with C:Genetics:
A:Introns: 1/1: 98/1: 114/1: 224/1: 329/1: 372/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F:337-306/Domain: immunoglobulin homology <IM1>
F:346-363/Domain: transmembrane #status predicted <TM>
F:364-399/Domain: intracellular #status predicted <INT>
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 1414; DB 1; Length 399;

Best Local Similarity 78.5%; Pred. No. 4,6e-77;
Matches 263; Conservative 30; Mismatches 36; Indels 6; Gaps 2;
Query 119 AKTTPSVYPLAPGCGPTGSSVTGLGVKGYPEPESVTVMNSSLSSSVHTFPALLQSG 178
1 AKTAPSVYPLAPVPCGGTSSVTGLGVKGYPEPVTLLTNSSSLSSGVTFFPAVLQSD 60
Db 1 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
179 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
61 LYTSSSVTVTSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 114
Qy 239 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 298
115 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 174
Qy 299 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 358
175 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 234
Db 359 PPAEQLSRKDVSLTCLVGVFNPDISVETWSNGHTEBNYKDTAPVLDSDGSYFYSKLN 418
235 PPPEEMTKKQVTLTCVTDPEMDIYEWMTNNGKTELNTPEVLDSDGSYFYSKLR 294
Qy 419 MKTSKMEKTDSEFCNVNHEGLKNTYLLKTTISRSPG 453
295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 329
Db 295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 329

RESULT 9
G2MSAM
Ig gamma-2a chain C region, secreted form (allele b) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Apr-1982 #sequence.revision 02-Apr-1982 #text.change 16-Jul-1999
C:Accession: A02153; A32656
R:Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A:Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and A:Reference number: A02153; MUID:82037861
A:Accession: A02153
A:Molecule type: mRNA
A:Residues: 1-335 <SCH>
A:Cross-references: GB:J00479
A:Experimental source: strain C57BL/6
R:Dognin, M.U.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A:Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc region A:Reference number: A32656; MUID:82037777
A:Accession: A32656
A:Molecule type: protein
A:Residues: 118-267, 'E', 269-328, 'G', 330-334 <DOG>
C:Comment: Lys-333 is removed posttranslationally.
C:Complex: The sequence differs from that of the allele, from BALB/c mice, at 15% of C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F:20-84/Domain: immunoglobulin homology <IM1>
F:98-118/Region: hinge
F:142-211/Domain: immunoglobulin homology <IM2>
F:248-315/Domain: immunoglobulin homology <IM3>
F:313/Disulfide bonds: Interchain (to light chain) #status predicted
F:27-82,149-209,255-313/Disulfide bonds: #status predicted
F:108,117/Disulfide bonds: interchain (to heavy chain) #status predicted
F:185/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 55.7%; Score 1385.5; DB 1; Length 335;
Best Local Similarity 77.1%; Pred. No. 1.6e-75;
Matches 259; Conservative 33; Mismatches 43; Indels 1; Gaps 1;
Query 119 AKTTPSVYPLAPGCGPTGSSVTGLGVKGYPEPESVTVMNSSLSSSVHTFPALLQSG 178
1 AKTAPSVYPLAPVPCGGTSSVTGLGVKGYPEPVTLLTNSSSLSSGVTFFPAVLQSD 60
Db 1 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
179 LYTMSSTVTPSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 238
61 LYTSSSVTVTSSVTPSQOTVCSVAHPASSSTTVYDKLLEPSGPISTINPCPCRCCHCPA 114
Qy 239 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 298
115 PNLGGSVTFEFPKIDVLMISLTPEKVTGVVDSSEDDPVOJISWFFVNNVEVHTAQTQT 174
Qy 299 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 358
175 HREDNSTIRVSTPLPIOHODMMSGKEPKCKVNNKDLPSPIERTISKIGLVRAPQVYIL 234
Db 359 PPAEQLSRKDVSLTCLVGVFNPDISVETWSNGHTEBNYKDTAPVLDSDGSYFYSKLN 418
235 PPPEEMTKKQVTLTCVTDPEMDIYEWMTNNGKTELNTPEVLDSDGSYFYSKLR 294
Qy 419 MKTSKMEKTDSEFCNVNHEGLKNTYLLKTTISRSPG 453
295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 329
Db 295 VEKNWERNYSYSCSVYHEGLHNHTTKSFRTPG 329

QY	179	LYTMSSTVYSSWSPQVYTCVAHBAASSTYADKKLEBGPSTINTPOCKECHKCA	238
Db	61	LYTSSSTVYTSNMWSPQITTCNAHBAASSTAKDKKIEBPVPL-TONPCPRHORPCAA	119
QY	239	PNEGCBSPVFLEPPNIKDVLMISLTPKRVTCVVVDVSEDDPDVQISFVNNAVVEHTAQOT	298
Db	120	PDLGGSPVFLEPPKIKDVLMISLSPKRVTCVVVDVSEDDPDVQISFVNNAVVEHTAQOT	179
QY	299	HREDYNSIRVYSLPLQIHDMMWGSKFEKCKVNNKCLPSPIETTSKIGIVRAPVYTL	358
Db	180	HREDNSTLRVYSLPLQIHDMMWGSKFEKCKVNNKCLPSPIETTSKIPGAPRAPVYTL	239
QY	359	PPPAEOLSRKDVSLTCLVGFNPGDISVEVETNSGHEENYKDTAPYLLDDSGSYFYISKLN	418
Db	240	PPPAEEMTKKEFSLTCLMITEGLPAEIAVDWTSNGRTQNKNTATYLLDDSGSYFYISKLR	299
QY	419	MKTSKMEKTDTSFCNNVHEGLKANYLYLKKTSRSBPK	454
Db	300	VOKSTWEGSLFACSVVHEVYLNHNLLTTKTSRSBLG	335

RESULT 10
PS0018
Ig gamma-2b chain C region - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
C:Accession: PS0018; B25941
R:Brueggemann, M.
Gene 74, 473-482, 1988
A>Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A:Reference number: PS0017; MUID:89232738
A:Accession: PS0018
A:Molecule type: DNA
A:Residues: 1-333 <BRU>
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A>Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397
A:Accession: B25941
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 227-333 <BR2>
C:Genetics:
A:Introns: 96/1; 117/1; 227/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: Immunoglobulin
;20-82/Domain: immunoglobulin homology <IMM>

Query Match	53.3%	Score 1326.5	DB 2	Length 333
Best Local Similarity	73.6%	Pred. No. 5.8e-72		
Matches 248	Conservative 34	Mismatches 50	Indels 5	Gaps 3
QY	119	AKTTPSVYPLAPGCGDITGSSVTGCLCYKGFPEPSMYTNMSSGLSSSVHFPALLOS	178	
		: : : : : : : : : : : : : : : : : : : : :		
DB	1	AQTAPSVYPLAPGCGDITGSSVTGCLCYKGFPEPSVITYNMSSGLSSDVHFPALLOS	60	
QY	179	LYTMSSSVTVSSSTPQSGVTCNVAPASSTVVDKLE-PSGPISITINCPCKECHKP	237	
		: : : : : : : : : : : : : : : : : : : :		
DB	61	LYTLTSSVT--SSWPSQFTVCNVANHPASSRFVDKKVERNGIG--HKCPICPCHCKP	116	
QY	238	APNLEGGSVFIFPPNIKDVLMI SLTPKVTQVYVDSEDDPDVQISWFINVNEVHTAQ	297	
		: : : : : : : : : : : : : : : : : : :		
DB	117	VPELGGSGSVFIFPPKPKDILLISQNAKVTQVYDSEBEPDQGSWFINVNEVHTAQ	176	
QY	298	THREDYNSTIVSVLPIQHODMMSGKEFKCKVNNKDLPSPIERTISIKGLVRAPOYTI	357	
		: : : : : : : : : : : : : : : : : :		
DB	177	PREQDYNSTIFVNSALPIQHODMMSGKEFKCKVNNKDALPSPIERTISPKGLVRRPOYV	236	
QY	358	LRPAEOLSRKDDSLTCLVNGPNPDISVEMVSNCHTEENTKDTAPVLVDSSQSYTI SKL	417	
		: : : : : : : : : : : : : : : : : :		
DB	237	MGPPLEOLTEQDVSTLCITLGSFLPNDIDVEMVSNCHIEKNKNTPEVVDSSQSFYTI SKL	296	

```

Qy      418 NMKTSKEWETDTSFSCNVRHGLKNYLLKTTISRSPGK 454
          :: :: :: :: :: :: :: :: :: :: :: :: ::
Db      297 NVRSRMDSRAPFVCSVYHGLHNHHVEKSISSRPgK 333

```

RESULT 11
S31459

Ig gamma-1 chain - sheep (fragment)
 C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S31459
 R:Patil, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31459
 A:Accession: S31459
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-472 <PAT>
 A:Cross-references: EMBL:X69797
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology
 C:Keywords: Immunoglobulin
 ;:277-346/Domain:Immunoglobulin homology <IMM>
 ;:277-346/Domain:Immunoglobulin homology <IMM>

Query Match	53.1%;	Score 1321.5;	DB 2;	Length 472;
Best Local Similarity	54.8%;	Pred. No. 1.7e-71;		
Matches 255;	Conservative 74;	Mismatches 115;	Indels 21;	Gaps 8;

QY	1	EVLOJGSEPELVKRGAGVMMKICRSATFFENYVHWKSHGSSLEWIGINPYGGSIF	60
Db	18	QVRQGESGPRSLATLLQTLVSTCHTISGSLNNYGVDMVROAPKRALEMLG-SGTDIED	76
QY	61	SPRKGAATLVTDKSSSTAYAMELRLTSEDSAVYYCAR-----RAGAY-YEDYWGOGT	113
Db	77	NPVLKSLSTLTKDTSKQVSLTSTVETEDTAYVYCARVDSDSHAFAYASYPFGGGL	136
QY	114	LVTSASATTPPSVYPLAPAGGGDTTGGSVTLGCLVKGEPESVYVNNMSGSLSSVHFPA	173
Db	137	ISVLASATTPPKVYPLPLSCGGDTSSSLVTLGCLVSSIMPEPVYVNNMSGSLTGVHFPA	196
QY	174	LLQ--SGELTSSSVYVPSSTWPSQTVVCSVAHPASSITVYVKKLEPSGPISTINPCP--PCK	231
Db	197	ILSSGLSLTSSVYVTAHVSAGQTFICNAVHAHPASSITVDKRVKPEG-----CPDPCK	248
QY	232	ECHKCAPNLGEGPSVFIFPPPNIKDVLAMISLTPKTCVYVDSSEDDPDVQISMFVANNVEY	291
Db	249	HC--RCPPPELPGSGSVIFPPKPKDVLITGTFEYVCCVYVDAQDDPEVQSMFVANNVEY	307
QY	292	HTAQTQHRREDYVNTIIVVSTLPIQIODMMGSGEFKCVKNNKDLPSPIETIKIGLVA	351
Db	308	RTAATKTRFEDFNSTFEVYVSAALPIQIODMTGGGEFKCVKNEALLPAPIVYITISRTGQAR	367
QY	352	APQVYLLPPPAEOLSRKDVSLTGLVVGFNPDGISVETWSNG--HTEENYKDPAPVLDSOG	409
Db	368	EPQYVYVLAPEQELSKSTLSVTCLVITGFYDYIAVEMQKQGESEDEKYGTTTSQILDAG	427
QY	410	SYFLSKLNMKTSKMEKTDTSFSCNVHREGKANKLYLKKTISRSGPK	454
Db	428	SYFLYSRLRVDKNSWQEGDGYACVYVMEALHNNYTKQKSIKPPGK	472

RESULT 12

Ig heavy chain precursor (B/MT 4A.17.H5.A5) - bovine
 N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 06-Jan-1995 #sequenceRevision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S22080; S06610; A31303
 R:Sanders, P. G.
 Submitted to the EMBL Data Library, November 1991
 A:Reference number: S22080
 A:Accession: S22080

Query Match	51.7%;	Score 1286.5;	DB 2;	Length 470;
Best Local Similarity	54.2%;	Pred. No. 2.1e-69;		
Matches 251; Conservative	70;	Mismatches 121;	Indels 21;	Gaps 8

RESULT 13

Cross-references: EMBL:X07189; NID:g57602; PIDN:CAA30169.1; PID:g663228

Query Match	48.4%	Score 1202.5	DB 2	Length 329
Best Local Similarity	68.2%	Pred. No. 1.3e-64		
Matches 229	Conservative 35	Mismatches 65	Indels 7	Gaps 4

```
Oy      419 MKTSKWEKTDSFSCNVRHEGLKNLYLKKTISRSPGK 454  
         : | : | : | : | : | : | : | : | :  
Db      294 VDTDSNMRRGDYYCSVHAEALNNHTQKNLSRSPGK 329
```

```
F:136-205/Domain: immunoglobulin homology <IM2>
F:242-309/Domain: immunoglobulin homology <IM3>
F:179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

Db 62 SSSLVTPSSQTVICNVAHPASKTELKRIEPR-----IPKPSTPPGSSCPPGN 115


```
QY 241 LEGGSEVFIEPPNKKDVLMSLTPKVTGVVVDSEDDPDVQISWFEVNNVEHTAQTOTHR 300
: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 116 ILGGSEVFIEPPNKKDVLMSLTPKVTGVVVDSEDDPDVQISWFEVNNVEHTAQTOTHR 175
QY 301 EDYNSTIRVSTLPIQHODWMSGKEFEKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 176 AQNSTFRVVSALPIQHODWMSGKEFEKCKVNNKALPAPIERTISKPKGRAQTPPOVYITLP 235
QY 361 PAEQLSRKDVSLTCLVGVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNK 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 PREQMSKKRVSLTCLVTFNFESEALISVEWERNGELEODYKNTPIILDSGTFLYSKLTVD 295
QY 421 TSKWEKTDSPSCNVREHGLKNYYLKKTTISRSPK 454
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 TDSWLQGEIFTCVSVHEALHNHTQKNLSRSPK 329
```

RESULT 15

G3MSM

Ig gamma-3 chain C region, membrane-bound form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999

C:Accession: A02156; A02155

R:Weis, J.A.; Word, C.J.; Kimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Blatt

EMBO J. 3, 2041-2046, 1984

A:Title: Structure analysis of the murine IgG3 constant region gene.

A:Reference number: A02156; MUID:85027161

A:Accession: A02156

A:Molecule type: DNA

A:Residues: 1-398 <WEI>

A:Cross-references: GB:J00451; NID:9194392; PIDN:AAB59655.1; PID:9194433

A>Note: the sequence was determined from the germline gene

R:Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R.

Nucleic Acids Res. 11, 6775-6785, 1983

A:Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene segment.

A:Reference number: A02155; MUID:84041483

A:Accession: A02155

A:Molecule type: DNA

A:Residues: 328-332, 'G', '334-341, 'Q', '343-387, 'F', '389-398 <KOM>

A:Cross-references: GB:K00688

A>Note: the sequence was determined from the germline gene

C:Genetics: 97/1: 113/1: 223/1: 328/1: 371/3

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin

F:19-83/Domain: immunoglobulin homology <IM1>

F:97-112/Region: hinge

F:136-205/Domain: immunoglobulin homology <IM2>

F:242-309/Domain: immunoglobulin homology <IM3>

F:346-362/Domain: transmembrane #status predicted <TM>

F:363-398/Domain: intracellular #status predicted <INT>

F:179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.6%; Score 1159; DB 1: Length 398;

Best Local Similarity 66.0%; Pred. No. 6.4e-62;

Matches 219; Conservative 33; Mismatches 74; Indels 6; Gaps 1;

```
QY 121 TTPPSVYPLAPCGDGTGSSVTLGCLVKGYPESVTWNSGSLSSSVHTFPALLQSGLY 180
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2 TTAPSVYPLVPCSDTSGSSVTLGCLVKGYPPEVTVMKNYCALSSGVTVSSVLSQSGFY 61
QY 181 TMSSTVYPSSTWPSQOTYCSVAHPASSITVDKLEPSGPSTINPCPPCKCHKCAPAN 240
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 62 SLSSTVYPSSTWPSQOTYCSVAHPASSITVDKLEPSGPSTINPCPPCKCHKCAPAN 115
QY 241 LEGGSEVFIEPPNKKDVLMSLTPKVTGVVVDSEDDPDVQISWFEVNNVEHTAQTOTHR 300
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 ILGGSEVFIEPPNKKDVLMSLTPKVTGVVVDSEDDPDVQISWFEVNNVEHTAQTOTHR 175
```

```
QY 301 EDYNSTIRVSTLPIQHODWMSGKEFEKCKVNNKDLPSPIERTISKIGLVRAPOVYITLP 360
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 176 AQNSTFRVVSALPIQHODWMSGKEFEKCKVNNKALPAPIERTISKPKGRAQTPPOVYITLP 235
QY 361 PAEQLSRKDVSLTCLVGVGNPDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNK 420
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 PREQMSKKRVSLTCLVTFNFESEALISVEWERNGELEODYKNTPIILDSGTFLYSKLTVD 295
QY 421 TSKWEKTDSPSCNVREHGLKNYYLKKTTISRSP 452
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 296 TDSWLQGEIFTCVSVHEALHNHTQKNLSRSP 327
```

Search completed: June 18, 2001, 15:32:47
Job time: 165 sec

